

0590  
1204

OIPE

## RAW SEQUENCE LISTING

DATE: 11/27/2001

PATENT APPLICATION: US/09/989,687

TIME: 14:19:56

Input Set : A:\seqlist\_1488.107000D

Output Set: N:\CRF3\11212001\I989687.raw

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7 <110> APPLICANT: Hastings, Gregg A.  
8 Ruben, Steven M.  
11 <120> TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
14 <130> FILE REFERENCE: 1488.107000D  
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/989,687 #  
C--> 20 <141> CURRENT FILING DATE: 2001-11-21  
23 <160> NUMBER OF SEQ ID NOS: 126  
26 <170> SOFTWARE: PatentIn Ver. 2.0  
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68 1 5 10 15  
70 ccc acg ctg ctg ctg ctc gcc gcg gcg cta ctg gcc gtg tcg gac gca 96  
71 Pro Thr Leu Leu Leu Ala Ala Ala Leu Leu Ala Val Ser Asp Ala  
72 20 25 30  
74 ctc ggg cgc ccc tcc gag gag gac gag gag cta gtg gtg ccg gag ctg 144  
75 Leu Gly Arg Pro Ser Glu Glu Asp Glu Glu Leu Val Val Pro Glu Leu  
76 35 40 45  
78 gag cgc gcc ccg gga cac ggg acc acg cgc ctc cgc ctg cac gcc ttt 192  
79 Glu Arg Ala Pro Gly His Gly Thr Thr Arg Leu Arg Leu His Ala Phe  
80 50 55 60  
82 gac cag cag ctg gat ctg gag ctg cgg ccc gac agc agc ttt ttg gcg 240  
83 Asp Gln Gln Leu Asp Leu Glu Leu Arg Pro Asp Ser Ser Phe Leu Ala  
84 65 70 75 80

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87 Pro Gly Phe Thr Leu Gln Asn Val Gly Arg Lys Ser Gly Ser Glu Thr
88      85      90      95
90 ccg ctt ccg gaa acc gac ctg gcg cac tgc ttc tac tcc ggc acc gtg 336
91 Pro Leu Pro Glu Thr Asp Leu Ala His Cys Phe Tyr Ser Gly Thr Val
92      100      105      110
94 aat ggc gat ccc agc tcg gct gcc gcc ctc agc ctc tgc gag ggc gtg 384
95 Asn Gly Asp Pro Ser Ser Ala Ala Ala Leu Ser Leu Cys Glu Gly Val
96      115      120      125
98 cgc ggc gcc ttc tac ctg ctg ggg gag gcg tat ttc atc cag ccg ctg 432
99 Arg Gly Ala Phe Tyr Leu Leu Gly Glu Ala Tyr Phe Ile Gln Pro Leu
100      130      135      140
102 ccc gcc gcc agc gag cgc ctc gcc acc gcc gcc cca ggg gag aag ccg 480
103 Pro Ala Ala Ser Glu Arg Leu Ala Thr Ala Ala Pro Gly Glu Lys Pro
104 145      150      155      160
106 ccg gca cca cta cag ttc cac ctc ctg cgg cgg aat cgg cag ggc gac 528
107 Pro Ala Pro Leu Gln Phe His Leu Leu Arg Arg Asn Arg Gln Gly Asp
108      165      170      175
110 gta ggc ggc acg tgc ggg gtc gtg gac gac gag ccc cgg ccg act ggg 576
111 Val Gly Gly Thr Cys Gly Val Val Asp Asp Glu Pro Arg Pro Thr Gly
112      180      185      190
114 aaa gcg gag acc gaa gac gag gac gaa ggg act gag ggc gag gac gaa 624
115 Lys Ala Glu Thr Glu Asp Glu Asp Glu Gly Thr Glu Gly Glu Asp Glu
116      195      200      205
118 ggg cct cag tgg tcg ccg cag gac ccg gca ctg caa ggc gta gga cag 672
119 Gly Pro Gln Trp Ser Pro Gln Asp Pro Ala Leu Gln Gly Val Gly Gln
120      210      215      220
122 ccc aca gga act gga agc ata aga aag aag cga ttt gtg tcc agt cac 720
123 Pro Thr Gly Thr Gly Ser Ile Arg Lys Lys Arg Phe Val Ser Ser His
124 225      230      235      240
126 cgc tat gtg gaa acc atg ctt gtg gca gac cag tcg atg gca gaa ttc 768
127 Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala Glu Phe
128      245      250      255
130 cac ggc agt ggt cta aag cat tac ctt ctc acg ttg ttt tcg gtg gca 816
131 His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser Val Ala
132      260      265      270
134 gcc aga ttg tac aaa cac ccc agc att cgt aat tca gtt agc ctg gtg 864
135 Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser Leu Val
136      275      280      285
138 gtg gtg aag atc ttg gtc atc cac gat gaa cag aag ggg ccg gaa gtg 912
139 Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu Val
140      290      295      300
142 acc tcc aat gct gcc ctc act ctg cgg aac ttt tgc aac tgg cag aag 960
143 Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln Lys
144 305      310      315      320
146 cag cac aac cca ccc agt gac cgg gat gca gag cac tat gac aca gca 1008
147 Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp Thr Ala
148      325      330      335
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152          340          345          350
154 ctt ggg atg gct gat gtt gga act gtg tgt gat ccg agc aga agc tgc 1104
155 Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg Ser Cys
156          355          360          365
158 tcc gtc ata gaa gat gat ggt tta caa gct gcc ttc acc aca gcc cat 1152
159 Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala His
160          370          375          380
162 gaa tta ggc cac gtg ttt aac atg cca cat gat gat gca aag cag tgt 1200
163 Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys Gln Cys
164 385          390          395          400
166 gcc agc ctt aat ggt gtg aac cag gat tcc cac atg atg gcg tca atg 1248
167 Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala Ser Met
168          405          410          415
170 ctt tcc aac ctg gac cac agc cag cct tgg tct cct tgc agt gcc tac 1296
171 Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser Ala Tyr
172          420          425          430
174 atg att aca tca ttt ctg gat aat ggt cat ggg gaa tgt ttg atg gac 1344
175 Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu Met Asp
176          435          440          445
178 aag cct cag aat ccc ata cag ctc cca ggc gat ctc cct ggc acc tcg 1392
179 Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly Thr Ser
180          450          455          460
182 tac gat gcc aac cgg cag tgc cag ttt aca ttt ggg gag gac tcc aaa 1440
183 Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Asp Ser Lys
184 465          470          475          480
186 cac tgc cct gat gca gcc agc aca tgt agc acc ttg tgg tgt acc ggc 1488
187 His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys Thr Gly
189          485          490          495
191 acc tct ggt ggg gtg ctg gtg tgt caa acc aaa cac ttc ccg tgg gcg 1536
192 Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro Trp Ala
193          500          505          510
195 gat ggc acc agc tgt gga gaa ggg aaa tgg tgt atc aac ggc aag tgt 1584
196 Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly Lys Cys
197          515          520          525
199 gtg aac aaa acc gac aga aag cat ttt gat acg cct ttt cat gga agc 1632
200 Val Asn Lys Thr Asp Arg Lys His Phe Asp Thr Pro Phe His Gly Ser
201          530          535          540
203 tgg gga atg tgg ggg cct tgg gga gac tgt tcg aga acg tgc ggt gga 1680
204 Trp Gly Met Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly
205 545          550          555          560
207 gga gtc cag tac acg atg agg gaa tgt gac aac cca gtc cca aag aat 1728
208 Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro Lys Asn
209          565          570          575
211 gga ggg aag tac tgt gaa ggc aaa cga gtg cgc tac aga tcc tgt aac 1776
212 Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser Cys Asn
213          580          585          590
215 ctt gag gac tgt cca gac aat aat gga aaa acc ttt aga gag gaa caa 1824
216 Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu Glu Gln

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217	595	600	605	
219	tgt gaa gca cac aac gag ttt tca aaa gct tcc ttt ggg agt ggg cct	1872		
220	Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly Pro			
221	610 615 620			
223	gcg gtg gaa tgg att ccc aag tac gct ggc gtc tca cca aag gac agg	1920		
224	Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys Asp Arg			
225	625 630 635 640			
227	tgc aag ctc atc tgc caa gcc aaa ggc att ggc tac ttc ttc gtt ttg	1968		
228	Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val Leu			
229	645 650 655			
231	cag ccc aag gtt gta gat ggt act cca tgt agc cca gat tcc acc tct	2016		
232	Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr Ser			
233	660 665 670			
235	gtc tgt gtg caa gga cag tgt gta aaa gct ggt tgt gat cgc atc ata	2064		
236	Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile Ile			
237	675 680 685			
239	gac tcc aaa aag aag ttt gat aaa tgt ggt gtt tgc ggg gga aat gga	2112		
240	Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn Gly			
241	690 695 700			
243	tct act tgt aaa aaa ata tca gga tca gtt act agt gca aaa cct gga	2160		
244	Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro Gly			
245	705 710 715 720			
247	tat cat gat atc atc aca att cca act gga gcc acc aac atc gaa gtg	2208		
248	Tyr His Asp Ile Ile Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu Val			
249	725 730 735			
252	aaa cag cgg aac cag agg gga tcc agg aac aat ggc agc ttt ctt gcc	2256		
253	Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu Ala			
254	740 745 750			
256	atc aaa gct gct gat ggc aca tat att ctt aat ggt gac tac act ttg	2304		
257	Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr Thr Leu			
258	755 760 765			
260	tcc acc tta gag caa gac att atg tac aaa ggt gtt gtc ttg agg tac	2352		
261	Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg Tyr			
262	770 775 780			
264	agc ggc tcc tct gcg gca ttg gaa aga att cgc agc ttt agc cct ctc	2400		
265	Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser Pro Leu			
266	785 790 795 800			
268	aaa gag ccc ttg acc atc cag gtt ctt act gtg ggc aat gcc ctt cga	2448		
269	Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala Leu Arg			
270	805 810 815			
272	cct aaa att aaa tac acc tac ttc gta aag aag aag aag gaa tct ttc	2496		
273	Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser Phe			
274	820 825 830			
276	aat gct atc ccc act ttt tca gca tgg gtc att gaa gag tgg ggc gaa	2544		
277	Asn Ala Ile Pro Thr Phe Ser Ala Trp Val Ile Glu Glu Trp Gly Glu			
278	835 840 845			
280	tgt tct aag tca tgt gaa ttg ggt tgg cag aga aga ctg gta gaa tgc	2592		
281	Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val Glu Cys			
282	850 855 860			

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286 865 870 875 880
288 cca gcc agc acc aga cct tgt gca gac cat ccc tgc ccc cag tgg cag 2688
289 Pro Ala Ser Thr Arg Pro Cys Ala Asp His Pro Cys Pro Gln Trp Gln
290 885 890 895
292 ctg ggg gag tgg tca tca tgt tct aag acc tgt ggg aag ggt tac aaa 2736
293 Leu Gly Glu Trp Ser Ser Cys Ser Lys Thr Cys Gly Lys Gly Tyr Lys
294 900 905 910
296 aaa aga agc ttg aag tgt ctg tcc cat gat gga ggg gtg tta tct cat 2784
297 Lys Arg Ser Leu Lys Cys Leu Ser His Asp Gly Gly Val Leu Ser His
298 915 920 925
300 gag agc tgt gat cct tta aag aaa cct aaa cat ttc ata gac ttt tgc 2832
301 Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp Phe Cys
302 930 935 940
304 aca atg gca gaa tgc agt taa gtggtttaag tgggtgttagc tttgaggcaa 2883
305 Thr Met Ala Glu Cys Ser
306 945 950
308 ggcaaagtga ggaagggctg gtgcagggaa agcaagaagg ctggagggat ccagcgtatc 2943
310 ttgccagtaa ccagtgaggt gtatcagtaa ggtgggatta tgggggtaga tagaaaagga 3003
312 gttgaatcat cagagtaaac tgccagtgtc aaatttgata ggatagttag tgaggattat 3063
W--> 315 taacctctga gcagtgatat agcataataa anccccgggc attattatta ttatttcttt 3123
317 tgttacatct attacaagtt tagaaaaaac aaagcaattg tcaaaaaaaaa aaaaaaaaaa 3183
319 aaaaaaaaaa aaaggcgggc cgctctagag gatccctcga ggggccaag cttacgcgtg 3243
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329 <213> ORGANISM: Homo sapiens
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338 Leu Gly Arg Pro Ser Glu Glu Asp Glu Glu Leu Val Val Pro Glu Leu
339 35 40 45
341 Glu Arg Ala Pro Gly His Gly Thr Thr Arg Leu Arg Leu His Ala Phe
342 50 55 60
344 Asp Gln Gln Leu Asp Leu Glu Leu Arg Pro Asp Ser Ser Phe Leu Ala
345 65 70 75 80
347 Pro Gly Phe Thr Leu Gln Asn Val Gly Arg Lys Ser Gly Ser Glu Thr
348 85 90 95
350 Pro Leu Pro Glu Thr Asp Leu Ala His Cys Phe Tyr Ser Gly Thr Val
351 100 105 110
353 Asn Gly Asp Pro Ser Ser Ala Ala Ala Leu Ser Leu Cys Glu Gly Val
354 115 120 125
356 Arg Gly Ala Phe Tyr Leu Leu Gly Glu Ala Tyr Phe Ile Gln Pro Leu
357 130 135 140
359 Pro Ala Ala Ser Glu Arg Leu Ala Thr Ala Ala Pro Gly Glu Lys Pro

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\seqlist\_1488.107000D

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L:17 M:270 C: Current Application Number differs, Replaced Application Number  
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:1533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:1732 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:9318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
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L:9652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
L:9654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
L:9656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
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L:9662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
L:9664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
L:9687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43  
L:9736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
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L:9821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
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L:9990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:9992 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
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L:10050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50  
L:10052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50

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L:10056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50  
L:10175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51  
L:10181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51